



OIEP

RAW SEQUENCE LISTING

DATE: 09/29/2003

PATENT APPLICATION: US/10/663,401

TIME: 14:36:33

Input Set : N:\CrF3\RULE60\10663401.raw.txt

Output Set: N:\CRF4\09292003\J663401.raw

ENTERED

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1 <110> APPLICANT: CHEN, Hong
2 <120> TITLE OF INVENTION: HUMAN GLUCOSE-6-PHOSPHATASE MOLECULES AND USES THEREOF
3 <130> FILE REFERENCE: 10147-33U1
4 <140> CURRENT APPLICATION NUMBER: US/10/663,401
5 <141> CURRENT FILING DATE: 2003-09-16
7 <150> PRIOR APPLICATION NUMBER: US/09/874,132
8 <151> PRIOR FILING DATE: 2001-06-04
9 <150> PRIOR APPLICATION NUMBER: US 09/586,511
10 <151> PRIOR FILING DATE: 2000-06-02
11 <160> NUMBER OF SEQ ID NOS: 27
12 <170> SOFTWARE: PatentIn Ver. 2.1
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 1138
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
18 <400> SEQUENCE: 1
19      aattcgcctt tcagctccaa ttgctctatg tttagaattg cctctttttc aagatggatt 60
20      tccttcacag gaatggagtg ctcataattc agcatttgca gaaggactac cgagcttact 120
21      acactttttc aaattttatg tccaatgttg gagaccccag gaatatcttt ttcattttatt 180
22      ttccactttg ttttcaattt aatcagacag ttggaaccaa gatgatatgg gtagcagtca 240
23      ttgggggattg gttaaatctt atattttaat ggatattatt tgggtcatcga ctttactggg 300
24      ggggtccaaga aactcagatt taccctaaatc actcaagtcc atgccttgaa cagttcccta 360
25      ctacatgtga aacagggtcca ggaagtccat ctggccatgc aatgggacga tcctgtgtct 420
26      ggtatgtcat ggtaaccgct gccctgagcc aactgtctg tgggatggat aagttctcta 480
27      tcaactctgca cagactgacc tgggtcatttc ttttgagtggt tttttggttg attcaaata 540
28      gtgtctgcat ctccagagta ttcatagcaa cacattttcc tcatcaagtt attcttgagg 600
29      taattggtgg catgctgggt gcagaggcct ttgaacacac tccaggcatc caaacggcca 660
30      gtctgggcac atacctgaag accaaccctt ttctcttctt gtttgcagtt ggcttttacc 720
31      tgcttcttag ggtgctcaac attgacctgc tgtggtccgt gcccatagcc aaaaagtgg 780
32      gtgctaaccg cgactggatc cacattgaca ccacgccttt tgctggactc gtgagaaacc 840
33      ttgggggtcct ctttggtctt ggctttgcaa tcaactcaga gatgttcctc ctgagctgcc 900
34      gagggggaaa taactacaca ctgagcttcc ggttgctctg tgccctgacc tcattgacaa 960
35      tactgcagct ctaccatttc ctccagatcc cgactcacga agagcattta ttttatgtgc 1020
36      tgtctttttg taaaagtgca tccattcccc taactgtggt tgctttcatt ccctactctg 1080
37      ttcatatgtt aatgaaacaa agcggaaaga agagtcagta gaaaaaaaaa aaaaaaaaa 1138
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 1065
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens
43 <400> SEQUENCE: 2
44      atggatttcc ttcacaggaa tggagtgtct ataattcagc atttgacaga ggactaccga 60
45      gcttactaca cttttctaaa ttttatgtcc aatgttgagg accccaggaa tatctttttc 120
46      atttattttc cactttgttt tcaatttaaa cagacagttg gaaccaagat gatatgggta 180

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47 gcagtcattg gggattgggt aaatcttata tttaaatgga tattatttgg tcatcgacct 240
48 tactgggtggg tccaagaaac tcagatttac ccaaactact caagtccatg ccttgaacag 300
49 ttccctacta catgtgaaac aggtccagga agtccatctg gccatgcaat gggcgcatcc 360
50 tgtgtctggt atgtcatggt aaccgctgcc ctgagccaca ctgtctgtgg gatggataag 420
51 ttctctatca ctctgcacag actgacctgg tcatttcttt ggagtgtttt ttggttgatt 480
52 caaatcagtg tctgcatctc cagagtattc atagcaacac attttcctca tcaagttatt 540
53 cttggagtaa ttggtggcat gctggtggca gaggcctttg aacacactcc aggcattcaa 600
54 acggccagtc tgggcacata cctgaagacc aacctctttc tcttcctggt tgcagttggc 660
55 ttttacctgc ttcttagggg gctcaacatt gacctgctgt ggtccgtgcc catagccaaa 720
56 aagtgggtgtg ctaaccccgga ctggatccac attgacacca cgccttttgc tggactcgtg 780
57 agaaaccttg gggctcctctt tggcttgggc tttgcaatca actcagagat gttcctcctg 840
58 agctgccgag ggggaaataa ctacacactg agcttccggt tgctctgtgc cttgacctca 900
59 ttgacaatac tgcagctcta ccatttcctc cagatcccga ctcacgaaga gcatttattt 960
60 tatgtgctgt ctttttgtaa aagtgcattc attcccctaa ctgtggttgc tttcattccc 1020
61 tactctgttc atatgttaat gaaacaaagc ggaaagaaga gtcag 1065

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63 <210> SEQ ID NO: 3

64 <211> LENGTH: 355

65 <212> TYPE: PRT

66 <213> ORGANISM: Homo sapiens

67 <400> SEQUENCE: 3

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68 Met Asp Phe Leu His Arg Asn Gly Val Leu Ile Ile Gln His Leu Gln
69 1 5 10 15
70 Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val
71 20 25 30
72 Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln
73 35 40 45
74 Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
75 50 55 60
76 Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
77 65 70 75 80
78 Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro
79 85 90 95
80 Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
81 100 105 110
82 Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr
83 115 120 125
84 Ala Ala Leu Ser His Thr Val Cys Gly Met Asp Lys Phe Ser Ile Thr
85 130 135 140
86 Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
87 145 150 155 160
88 Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
89 165 170 175
90 His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
91 180 185 190
92 Phe Glu His Thr Pro Gly Ile Gln Thr Ala Ser Leu Gly Thr Tyr Leu
93 195 200 205
94 Lys Thr Asn Leu Phe Leu Phe Leu Phe Ala Val Gly Phe Tyr Leu Leu
95 210 215 220
96 Leu Arg Val Leu Asn Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys

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```

97      225      230      235      240
98      Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Thr Thr Pro Phe
99              245      250      255
100     Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala
101              260      265      270
102     Ile Asn Ser Glu Met Phe Leu Leu Ser Cys Arg Gly Gly Asn Asn Tyr
103              275      280      285
104     Thr Leu Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Ile Leu
105              290      295      300
106     Gln Leu Tyr His Phe Leu Gln Ile Pro Thr His Glu Glu His Leu Phe
107     305              310      315      320
108     Tyr Val Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Thr Val Val
109              325      330      335
110     Ala Phe Ile Pro Tyr Ser Val His Met Leu Met Lys Gln Ser Gly Lys
111              340      345      350
112     Lys Ser Gln
113              355
115 <210> SEQ ID NO: 4
116 <211> LENGTH: 355
117 <212> TYPE: PRT
118 <213> ORGANISM: Mus musculus
119 <400> SEQUENCE: 4
120     Met Asp Phe Leu His Arg Ser Gly Val Leu Ile Ile His His Leu Gln
121     1      5      10      15
122     Glu Asp Tyr Arg Thr Tyr Tyr Gly Phe Leu Asn Phe Met Ser Asn Val
123              20      25      30
124     Gly Asp Pro Arg Asn Ile Phe Ser Ile Tyr Phe Pro Leu Trp Phe Gln
125     35      40      45
126     Leu Asn Gln Asn Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
127     50      55      60
128     Asp Trp Phe Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
129     65      70      75      80
130     Tyr Trp Trp Ile Gln Glu Thr Glu Ile Tyr Pro Asn His Ser Ser Pro
131              85      90      95
132     Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
133              100      105      110
134     Ser Gly His Ala Met Gly Ser Ser Cys Val Trp Tyr Val Met Val Thr
135              115      120      125
136     Ala Ala Leu Ser Tyr Thr Ile Ser Arg Met Glu Glu Ser Ser Val Thr
137     130      135      140
138     Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
139     145      150      155      160
140     Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
141              165      170      175
142     His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
143              180      185      190
144     Phe Glu His Thr Pro Gly Val His Met Ala Ser Leu Ser Val Tyr Leu
145     195      200      205
146     Lys Thr Asn Val Phe Leu Phe Leu Phe Ala Leu Gly Phe Tyr Leu Leu

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Output Set: N:\CRF4\09292003\J663401.raw

```

147      210      215      220
148      Leu Arg Leu Phe Gly Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
149      225      230      235      240
150      Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Ser Thr Pro Phe
151      245      250      255
152      Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala
153      260      265      270
154      Ile Asn Ser Glu Met Phe Leu Arg Ser Cys Gln Gly Glu Asn Gly Thr
155      275      280      285
156      Lys Pro Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Thr Met
157      290      295      300
158      Gln Leu Tyr Arg Phe Ile Lys Ile Pro Thr His Ala Glu Pro Leu Phe
159      305      310      315      320
160      Tyr Leu Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Met Val Val
161      325      330      335
162      Ala Leu Ile Pro Tyr Cys Val His Met Leu Met Arg Pro Gly Asp Lys
163      340      345      350
164      Lys Thr Lys
165      355
167 <210> SEQ ID NO: 5
168 <211> LENGTH:
169 <212> TYPE:
170 <213> ORGANISM:
171 <400> SEQUENCE: 5
W--> 172      000
174 <210> SEQ ID NO: 6
175 <211> LENGTH:
176 <212> TYPE:
177 <213> ORGANISM:
178 <400> SEQUENCE: 6
W--> 179      000
181 <210> SEQ ID NO: 7
182 <211> LENGTH:
183 <212> TYPE:
184 <213> ORGANISM:
185 <400> SEQUENCE: 7
W--> 186      000
188 <210> SEQ ID NO: 8
189 <211> LENGTH:
190 <212> TYPE:
191 <213> ORGANISM:
192 <400> SEQUENCE: 8
W--> 193      000
195 <210> SEQ ID NO: 9
196 <211> LENGTH:
197 <212> TYPE:
198 <213> ORGANISM:
199 <400> SEQUENCE: 9
W--> 200      000

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Input Set : N:\Crf3\RULE60\10663401.raw.txt

Output Set: N:\CRF4\09292003\J663401.raw

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202 <210> SEQ ID NO: 10
203 <211> LENGTH:
204 <212> TYPE:
205 <213> ORGANISM:
206 <400> SEQUENCE: 10
W--> 207      000
209 <210> SEQ ID NO: 11
210 <211> LENGTH:
211 <212> TYPE:
212 <213> ORGANISM:
213 <400> SEQUENCE: 11
W--> 214      000
216 <210> SEQ ID NO: 12
217 <211> LENGTH:
218 <212> TYPE:
219 <213> ORGANISM:
220 <400> SEQUENCE: 12
W--> 221      000
223 <210> SEQ ID NO: 13
224 <211> LENGTH:
225 <212> TYPE:
226 <213> ORGANISM:
227 <400> SEQUENCE: 13
W--> 228      000
230 <210> SEQ ID NO: 14
231 <211> LENGTH:
232 <212> TYPE:
233 <213> ORGANISM:
234 <400> SEQUENCE: 14
W--> 235      000
237 <210> SEQ ID NO: 15
238 <211> LENGTH:
239 <212> TYPE:
240 <213> ORGANISM:
241 <400> SEQUENCE: 15
W--> 242      000
244 <210> SEQ ID NO: 16
245 <211> LENGTH:
246 <212> TYPE:
247 <213> ORGANISM:
248 <400> SEQUENCE: 16
W--> 249      000
251 <210> SEQ ID NO: 17
252 <211> LENGTH:
253 <212> TYPE:
254 <213> ORGANISM:
255 <400> SEQUENCE: 17
W--> 256      000
258 <210> SEQ ID NO: 18
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/663,401

DATE: 09/29/2003
TIME: 14:36:34

Input Set : N:\Crf3\RULE60\10663401.raw.txt
Output Set: N:\CRF4\09292003\J663401.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10663401.raw.txt

Output Set: N:\CRF4\09292003\J663401.raw

L:172 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:179 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:186 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:193 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:200 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:207 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:214 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:221 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:228 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:235 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:242 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:249 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:256 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:263 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:270 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:277 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:284 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (21) SEQUENCE: